



SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko
Kobayashi, Midori

<120> HUMAN PROTEINS HAVING SECRETORY SIGNAL
SEQUENCES AND DNAs ENCODING THESE PROTEINS

<130> GIN-6/040PUS

<140> US 09/254,760

<141> 1999-04-16

<150> JP 8/243,060

<151> 1996-09-13

<150> PCT/JP97/03239

<151> 1997-09-12

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Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His
50 55 60
Arg Ser Arg Met Pro Lys Arg Glu Gly Glu Glu Val Trp Glu Asp Phe
65 70 75 80
Leu Tyr Arg Ser Arg Ser Asn Lys Gly Asp Leu Tyr His Pro Lys Ala
85 90 95
Pro Pro Ser Val Cys Gln Pro Arg Glu Glu Met Gly Ser Gly Val His
100 105 110
Gln Leu Phe Gly Asp Glu Leu Gly Trp Arg Val Leu Glu Pro Glu Leu
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85 90
 Ala His Leu Ala Ser Ile Leu Ser Leu Lys Glu Ala Ser Thr Ile Ala
 65 70 75 80
 Glu Tyr Ile Ser Gly Tyr Gln Arg Ser Gln Ile Ile Thr Ile Gly Leu
 85 90 95
 His Asp Pro Gln Lys Arg Gln Gln Trp Gln Trp Ile Asp Gly Ala Met
 100 105 110
 Tyr Leu Tyr Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His
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 35 40 45
 Ala Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu
 50 55 60
 Gln Ile Val Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Glu Asp Asn
 65 70 75 80
 Pro Thr Pro Gly Ile Val Ile Asn Arg Pro Asn Gly Thr Asp Val Tyr
 85 90 95
 Gln Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Pro Gln Asn
 100 105 110
 Phe Leu Ala Val Leu Arg Gly Asp Ala Glu Ala Val Lys Gly Ile Gly
 115 120 125
 Ser Gly Lys Val Leu Lys Ser Gly Pro Gln Asp His Val Phe Ile Tyr
 130 135 140
 Phe Thr Asp His Gly Ser Thr Gly Ile Leu Val Ile His Asn Ala Arg
 145 150 155
 Ser His Val Lys Arg Ser Asn Ala Thr Ile His Tyr Ser Tyr Lys His
 160 165 170
 Lys Met Tyr Arg Lys Met Val Ile Tyr Ile Ala Ala Tyr Glu Ser Gly
 175 180 185 190
 Ser Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr
 195 200 205
 Ala Ala Asn Ile Asn Glu Ser Tyr Ala Tyr Tyr Tyr Arg Glu Lys
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225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

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 290 295 300
 Thr Pro Ser Pro Asp Val Pro Leu Thr Ile Met Lys Arg Lys Leu Met
 305 310 315 320
 Asn Thr Asn Asp Leu Glu Glu Ser Arg Gln Leu Thr Glu Glu Ile Gln
 325 330 335
 Arg His Leu Asp Tyr Glu Tyr Ala Leu Arg His Leu Tyr Val Leu Val
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 Asp His Val Cys Leu Gly His Tyr
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 35 40 45
 His Ser Phe Ser His Asn Val Gly Pro Gly Asp Lys Tyr Thr Cys Met
 50 55 60
 Phe Thr Tyr Ala Ser Gln Gly Gly Thr Asn Glu Gln Trp Gln Met Ser
 65 70 75 80
 Leu Gly Thr Ser Glu Asp His Gln His Phe Thr Cys Thr Ile Trp Arg
 85 90 95
 Pro Gln Gly Lys Ser Tyr Leu Tyr Phe Thr Gln Phe Lys Ala Glu Val
 100 105 110
 Arg Gly Ala Glu Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 115 120 125
 Glu Arg Glu Ser Asp Val Pro Leu Lys Thr Glu Glu Phe Glu Val Thr
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 145 150 155 160
 Lys Leu Val Ile Val Ala Tyr Ala Ser Arg His Arg Leu
 165 170

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 35 40 45
 Leu Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met
 50 55 60
 Lys Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His
 65 70 75 80
 Arg Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln
 85 90 95
 Ser Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg
 100 105 110
 Arg Phe Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro
 115 120 125
 Ala Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg
 130 135 140
 Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val
 145 150 155 160
 Arg Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu
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 Pro Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn
 180 185 190
 Leu Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile
 195 200 205
 Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu
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 Ala Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala
 225 230 235 240
 Val Ser Gln Leu Arg Ser Gln Gly Ser Tyr Ile Tyr His Gly His Ala
 245 250 255 260
 Asp Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala
 265 270
 Val Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro
 275 280 285
 Asn Tyr Gln Arg Cys Ala Pro Ile Tyr Asn Asn Arg Ile Thr Asn Ile
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 Gly Ala Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val
 385 390 395 400
 Cys Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly
 405 410 415
 Phe Thr Gly Leu Thr Tyr Ala Asn Pro Gln Gly Cys His Arg Cys Asp
 420 425 430
 Cys Asn Ile Leu Gly Ser Arg Arg Asp Met Pro Cys Asp Glu Glu Ser
 435 440 445
 Gly Arg Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln
 450 455 460
 Cys Ala Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro
 465 470 475 480
 Cys Ala Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe
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 Thr Gly Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser
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 Gly Cys Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr
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 Gly Pro Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro
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 Val Cys Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu
 580 585 590
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 595 600 605
 Leu Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile
 610 615 620
 Leu Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser
 625 630 635 640
 Pro Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu
 645 650 655
 Ser Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu
 660 665 670
 Ala Gln Thr Leu Ser Leu Ile Arg Asp Leu Ala Ser Leu Asp Arg Ser
 675 680 685
 Phe Asn Gly Leu Leu Thr Met Tyr Ala Asn Lys Arg Ala Ala Ile Gln
 690 695
 Tyr Ile Ser Ser Ala Arg Phe Asn Gly Ala Phe Arg Met Leu Ser Thr
 700 705 710 715 720
 Ala Tyr Gln Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser
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 Arg Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Gln Ala Gln Arg Leu
 740 745 750
 Val Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Ile Lys Leu Val

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 35 40 45
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 65 70 75 80
 Arg Ala Ala Cys Thr Val Phe Thr Ala Thr Ala Ser Thr Arg Thr Trp
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 35 40 45
 Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 50 55 60
 Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 65 70 75 80
 Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
 85 90 95
 Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
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 Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile
 115 120 125
 Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Thr Gly Arg
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 Leu Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr Ala Leu
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462

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gatgctcaga gttttgatta tgaccatgat gccttcttgg gtgctgaaga agcaaaagac 180
tttgatcagc tgacaccaga agagagcaag gaaaggcttg gaaagattgt aagtaaaata 240
gatgcgcaca aggaagggtt tgtcactgtg gatgagctca aagaatggat taaatttgca 300
caaaagccgt ggatttacga ggatgtagag cgacagtggg aggggcctga cctcaatgag 360
gacggcctcg ttctctggga ggagtataaa aatgccacct accgtacgt tttagatgat 420
ccagatcctg atgatggatt taactataaa cagatgatgg ttagagatga ggggaggttt 480
aaaatggcag acaaggatgg agacctcatt gccaccaagg aggagttcac agcttctctg 540
caccctgagg agtatgacta catgaaagat atagtagtac aggaacaaat ggaagatata 600
gataagaatg ctgatggtt cattgatcta gaagagtata ttggtgacat gtacagccat 660
gatgggaata ctgatgagc agaatgggta aagacagagc gagagcagtt tgttgagttt 720
cgggataaga accgtgatgg gaagatggac aagggaagaga ccaaagactg gatccttccc 780
tcagactatg atcatgcaga ggcagaagcc aggcacctgg tctatgaatc agacccaaac 840
aaggatggca agcttaccac ggaggagatc gttgacaagt atgaattatt tgttggcagc 900
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tgcatgggtt acttcaggaa gctgaggaa cggctctgat ccgagctcga gtgtcagttc 180
tacgaaaacg gagccacact ggcattctat ctgagtttaa aggaagccag caccatagca 240
gagtcacata gtggctatca gagaagccag ccgatatgga ttggcctgca cgacccacag 300
aagaggagag agtggcagtg gatggatggg accatctatc tatcacagtc ctggtctggc 360
atgctctatg atgggacaa gactgtggtt gattgagct gattatgaa gttttgact 420
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<213> Homo sapiens

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tgcatgggtt acttcaggaa gctgaggaa cggctctgat ccgagctcga gtgtcagttc 180
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gagtcacata gtggctatca gagaagccag ccgatatgga ttggcctgca cgacccacag 300
aagaggagag agtggcagtg gatggatggg accatctatc tatcacagtc ctggtctggc 360
atgctctatg atgggacaa gactgtggtt gattgagct gattatgaa gttttgact 420
tgggagatca atgtttaa gattttaa gattttaa gattttaa gattttaa 480
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1000

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<210> 15

<211> 219

<212> DNA

<213> Homo sapiens

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<210> 16

Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* and *Agaricus bisporus* spores. The concentration of the spores was 10⁶ spores/ml (a), 10⁷ spores/ml (b), 10⁸ spores/ml (c), 10⁹ spores/ml (d), 10¹⁰ spores/ml (e), 10¹¹ spores/ml (f), 10¹² spores/ml (g), 10¹³ spores/ml (h), 10¹⁴ spores/ml (i), 10¹⁵ spores/ml (j), 10¹⁶ spores/ml (k), 10¹⁷ spores/ml (l), 10¹⁸ spores/ml (m), 10¹⁹ spores/ml (n), 10²⁰ spores/ml (o), 10²¹ spores/ml (p), 10²² spores/ml (q), 10²³ spores/ml (r), 10²⁴ spores/ml (s), 10²⁵ spores/ml (t), 10²⁶ spores/ml (u), 10²⁷ spores/ml (v), 10²⁸ spores/ml (w), 10²⁹ spores/ml (x), 10³⁰ spores/ml (y), 10³¹ spores/ml (z), 10³² spores/ml (aa), 10³³ spores/ml (ab), 10³⁴ spores/ml (ac), 10³⁵ spores/ml (ad), 10³⁶ spores/ml (ae), 10³⁷ spores/ml (af), 10³⁸ spores/ml (ag), 10³⁹ spores/ml (ah), 10⁴⁰ spores/ml (ai), 10⁴¹ spores/ml (aj), 10⁴² spores/ml (ak), 10⁴³ spores/ml (al), 10⁴⁴ spores/ml (am), 10⁴⁵ spores/ml (an), 10⁴⁶ spores/ml (ao), 10⁴⁷ spores/ml (ap), 10⁴⁸ spores/ml (aq), 10⁴⁹ spores/ml (ar), 10⁵⁰ spores/ml (as), 10⁵¹ spores/ml (at), 10⁵² spores/ml (au), 10⁵³ spores/ml (av), 10⁵⁴ spores/ml (aw), 10⁵⁵ spores/ml (ax), 10⁵⁶ spores/ml (ay), 10⁵⁷ spores/ml (az), 10⁵⁸ spores/ml (ba), 10⁵⁹ spores/ml (bb), 10⁶⁰ spores/ml (bc), 10⁶¹ spores/ml (bd), 10⁶² spores/ml (be), 10⁶³ spores/ml (bf), 10⁶⁴ spores/ml (bg), 10⁶⁵ spores/ml (bh), 10⁶⁶ spores/ml (bi), 10⁶⁷ spores/ml (bj), 10⁶⁸ spores/ml (bk), 10⁶⁹ spores/ml (bl), 10⁷⁰ spores/ml (bm), 10⁷¹ spores/ml (bn), 10⁷² spores/ml (bo), 10⁷³ spores/ml (bp), 10⁷⁴ spores/ml (bq), 10⁷⁵ spores/ml (br), 10⁷⁶ spores/ml (bs), 10⁷⁷ spores/ml (bt), 10⁷⁸ spores/ml (bu), 10⁷⁹ spores/ml (bv), 10⁸⁰ spores/ml (bw), 10⁸¹ spores/ml (bx), 10⁸² spores/ml (by), 10⁸³ spores/ml (bz), 10⁸⁴ spores/ml (ca), 10⁸⁵ spores/ml (cb), 10⁸⁶ spores/ml (cc), 10⁸⁷ spores/ml (cd), 10⁸⁸ spores/ml (ce), 10⁸⁹ spores/ml (cf), 10⁹⁰ spores/ml (cg), 10⁹¹ spores/ml (ch), 10⁹² spores/ml (ci), 10⁹³ spores/ml (cj), 10⁹⁴ spores/ml (ck), 10⁹⁵ spores/ml (cl), 10⁹⁶ spores/ml (cm), 10⁹⁷ spores/ml (cn), 10⁹⁸ spores/ml (co), 10⁹⁹ spores/ml (cp), 10¹⁰⁰ spores/ml (cq), 10¹⁰¹ spores/ml (cr), 10¹⁰² spores/ml (cs), 10¹⁰³ spores/ml (ct), 10¹⁰⁴ spores/ml (cu), 10¹⁰⁵ spores/ml (cv), 10¹⁰⁶ spores/ml (cw), 10¹⁰⁷ spores/ml (cx), 10¹⁰⁸ spores/ml (cy), 10¹⁰⁹ spores/ml (cz), 10¹¹⁰ spores/ml (da), 10¹¹¹ spores/ml (db), 10¹¹² spores/ml (dc), 10¹¹³ spores/ml (dd), 10¹¹⁴ spores/ml (de), 10¹¹⁵ spores/ml (df), 10¹¹⁶ spores/ml (dg), 10¹¹⁷ spores/ml (dh), 10¹¹⁸ spores/ml (di), 10¹¹⁹ spores/ml (dj), 10¹²⁰ spores/ml (dk), 10¹²¹ spores/ml (dl), 10¹²² spores/ml (dm), 10¹²³ spores/ml (dn), 10¹²⁴ spores/ml (do), 10¹²⁵ spores/ml (dp), 10¹²⁶ spores/ml (dq), 10¹²⁷ spores/ml (dr), 10¹²⁸ spores/ml (ds), 10¹²⁹ spores/ml (dt), 10¹³⁰ spores/ml (du), 10¹³¹ spores/ml (dv), 10¹³² spores/ml (dw), 10¹³³ spores/ml (dx), 10¹³⁴ spores/ml (dy), 10¹³⁵ spores/ml (dz), 10¹³⁶ spores/ml (ea), 10¹³⁷ spores/ml (eb), 10¹³⁸ spores/ml (ec), 10¹³⁹ spores/ml (ed), 10¹⁴⁰ spores/ml (ee), 10¹⁴¹ spores/ml (ef), 10¹⁴² spores/ml (eg), 10¹⁴³ spores/ml (eh), 10¹⁴⁴ spores/ml (ei), 10¹⁴⁵ spores/ml (ej), 10¹⁴⁶ spores/ml (ek), 10¹⁴⁷ spores/ml (el), 10¹⁴⁸ spores/ml (em), 10¹⁴⁹ spores/ml (en), 10¹⁵⁰ spores/ml (eo), 10¹⁵¹ spores/ml (ep), 10¹⁵² spores/ml (eq), 10¹⁵³ spores/ml (er), 10¹⁵⁴ spores/ml (es), 10¹⁵⁵ spores/ml (et), 10¹⁵⁶ spores/ml (eu), 10¹⁵⁷ spores/ml (ev), 10¹⁵⁸ spores/ml (ew), 10¹⁵⁹ spores/ml (ex), 10¹⁶⁰ spores/ml (ey), 10¹⁶¹ spores/ml (ez), 10¹⁶² spores/ml (fa), 10¹⁶³ spores/ml (fb), 10¹⁶⁴ spores/ml (fc), 10¹⁶⁵ spores/ml (fd), 10¹⁶⁶ spores/ml (fe), 10¹⁶⁷ spores/ml (ff), 10¹⁶⁸ spores/ml (fg), 10¹⁶⁹ spores/ml (fh), 10¹⁷⁰ spores/ml (fi), 10¹⁷¹ spores/ml (fj), 10¹⁷² spores/ml (fk), 10¹⁷³ spores/ml (fl), 10¹⁷⁴ spores/ml (fm), 10¹⁷⁵ spores/ml (fn), 10¹⁷⁶ spores/ml (fo), 10¹⁷⁷ spores/ml (fp), 10¹⁷⁸ spores/ml (fq), 10¹⁷⁹ spores/ml (fr), 10¹⁸⁰ spores/ml (fs), 10¹⁸¹ spores/ml (ft), 10¹⁸² spores/ml (fu), 10¹⁸³ spores/ml (fv), 10¹⁸⁴ spores/ml (fw), 10¹⁸⁵ spores/ml (fx), 10¹⁸⁶ spores/ml (fy), 10¹⁸⁷ spores/ml (fz), 10¹⁸⁸ spores/ml (ga), 10¹⁸⁹ spores/ml (gb), 10¹⁹⁰ spores/ml (gc), 10¹⁹¹ spores/ml (gd), 10¹⁹² spores/ml (ge), 10¹⁹³ spores/ml (gf), 10¹⁹⁴ spores/ml (gg), 10¹⁹⁵ spores/ml (gh), 10¹⁹⁶ spores/ml (gi), 10¹⁹⁷ spores/ml (gj), 10¹⁹⁸ spores/ml (gk), 10¹⁹⁹ spores/ml (gl), 10²⁰⁰ spores/ml (gm), 10²⁰¹ spores/ml (gn), 10²⁰² spores/ml (go), 10²⁰³ spores/ml (gp), 10²⁰⁴ spores/ml (gq), 10²⁰⁵ spores/ml (gr), 10²⁰⁶ spores/ml (gs), 10²⁰⁷ spores/ml (gt), 10²⁰⁸ spores/ml (gu), 10²⁰⁹ spores/ml (gv), 10²¹⁰ spores/ml (gw), 10²¹¹ spores/ml (gx), 10²¹² spores/ml (gy), 10²¹³ spores/ml (gz), 10²¹⁴ spores/ml (ha), 10²¹⁵ spores/ml (hb), 10²¹⁶ spores/ml (hc), 10²¹⁷ spores/ml (hd), 10²¹⁸ spores/ml (he), 10²¹⁹ spores/ml (hf), 10²²⁰ spores/ml (hg), 10²²¹ spores/ml (hh), 10²²² spores/ml (hi), 10²²³ spores/ml (hj), 10²²⁴ spores/ml (hk), 10²²⁵ spores/ml (hl), 10²²⁶ spores/ml (hm), 10²²⁷ spores/ml (hn), 10²²⁸ spores/ml (ho), 10²²⁹ spores/ml (hp), 10²³⁰ spores/ml (hq), 10²³¹ spores/ml (hr), 10²³² spores/ml (hs), 10²³³ spores/ml (ht), 10²³⁴ spores/ml (hu),

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1. The data in this file were generated by the program "seq" (version 1.0) which is part of the "seq" package (version 1.0) available from the NCBI. The data were generated on 10/10/90.

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agctacatcc tcagggtagy aggaag atg gct tcc aga agc atg cgg ctg ctg 173
Met Ala Ser Arg Ser Met Arg Leu Leu

1 5

cra ttg ctg agc tgc ctg gcc aaa aca gga gtc ctg ggt gat atc atc 221
Leu Leu Leu Ser Cys Leu Ala Lys Thr Gly Val Leu Gly Asp Ile Ile
10 15 20 25

atg aga ccc agc tgt gct cct gga tgg ttt tac cac aag tcc aat tgc 269
Met Arg Pro Ser Cys Ala Pro Gly Trp Phe Tyr His Lys Ser Asn Cys
30 35 40

tat ggt tac ttc agg aag ctg agg aac tgg tct gat gcc gag ctg gag 317
Tyr Gly Tyr Phe Arg Lys Leu Arg Asn Trp Ser Asp Ala Glu Leu Glu
45 50 55

tgt cag tct tac gga aac gga gcc cac ctg gca tct atc ctg agt tta 365
Cys Gln Ser Tyr Gly Asn Gly Ala His Leu Ala Ser Ile Leu Ser Leu
60 65 70

aag gaa gcc agc acc ata gca gag tac ata agt gcc tat cag aga agc 413
Lys Glu Ala Ser Thr Ile Ala Glu Tyr Ile Ser Gly Tyr Gln Arg Ser
75 80 85

cag ccg ata tgg att ggc ctg cac gac cca cag aag agg cag cag tgg 461
Gln Pro Ile Trp Ile Gly Leu His Asp Pro Gln Lys Arg Gln Gln Trp
90 95 100 105

cag tgg att gat ggg gcc atg tat ctg tac aga tcc tgg tct gcc aag 509
Gln Trp Ile Asp Gly Ala Met Tyr Leu Tyr Arg Ser Trp Ser Gly Lys
110 115 120

tcc atg ggt ggg aac aag cac tgt gct gag atg agc tcc aat aac aac 557
Ser Met Gly Gly Asn Lys His Cys Ala Glu Met Ser Ser Asn Asn Asn
135 140 145

ttt tta att ttt att att att att att att att att att att att att 617
Ile Leu Thr Trp Ser Ser Ala Ala Cys Asn Lys Arg His His Ile Leu
160 165 170

tgc aag tac cga cca tagagcaaga atcaagattc tgctaacctc tgcacagccc 660
Cys Lys Tyr Arg Pro
175

atctttttt cttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 727

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<223> misc feature
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 Met
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gtt tgg aaa gta ggt gta ttc ctc agt gtg gac ctg ggc atc ggt gac 167
 Val Trp Lys Val Ala Val Phe Leu Ser Val Ala Leu Gly Ile Gly Ala
 5 10 15

gtt cct ata gat gat cct gaa gat gga ggt aag cac tgg gtg gta atc 215
 Val Pro Ile Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val Ile
 20 25 30

gtg gca ggt tca aat ggc tgg tat aat tat agg cac cag gca gac ggc 263
 Val Ala Gly Ser Asn Gly Trp Tyr Asn Tyr Arg His Gln Ala Asp Ala
 35 40 45

tgc cat gac tac cag atc att cac cgc aat ggg att cct gac gaa cag 311
 Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu Gln
 50 55 60 65

atc gtt gta atg atg tac gat gac att gct tac tct gaa gac aat gac 359
 Ile Val Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Gln Asp Asn Ile
 70 75 80 85

atc gta gta att gta att gta att gta att gta att gta att gta att 407
 Ile Trp Gly Ile Val Ile Asn Asn Ile Asn Gly Thr Asp Val Tyr Gln
 90 95 100 105

gga gta cgt aat gac tac aat gga gac tat gta att gca gac aat ttc 455
 Gly Val Pro Lys Asp Tyr Thr Gly Gln Asp Val Thr Pro Gln Asn Ile
 110 115 120 125

atc gta gta att gta att gta att gta att gta att gta att gta att 503
 Ile Trp Gly Ile Val Ile Asn Asn Ile Asn Gly Thr Asp Val Tyr Gln
 130 135 140 145

61
 (ex)

Thr Asp His Gly Ser Thr Gly Ile Leu Val Phe Ile Asn Gln Arg Leu	647
150 155 160	
His Val Lys Asp Leu Asn Glu Phe Ile His Tyr Met Tyr Lys His Lys	
165 170 175	
Met Tyr Arg Lys Met Val Phe Tyr Ile Glu Ala Cys Glu Ser Gly Ser	695
180 185 190	
Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr Ala	743
195 200 205	
Ala Asn Pro Arg Glu Ser Ser Tyr Ala Cys Tyr Tyr Met Gln Lys Arg	791
210 215 220 225	
Ser Thr Tyr Leu Gly Asp Trp Tyr Ser Val Asn Trp Met Glu Asp Ser	839
230 235 240	
Asp Val Glu Asp Leu Thr Lys Glu Thr Leu His Lys Gln Tyr His Leu	887
245 250 255	
Val Lys Ser His Thr Asn Thr Ser His Val Met Gln Tyr Gly Asn Lys	935
260 265 270	
Thr Ile Ser Thr Met Lys Val Met Gln Phe Gln Gly Met Lys Arg Lys	983
275 280 285	
Ala Ser Ser Pro Val Pro Leu Pro Pro Val Thr His Leu Asp Leu Thr	1031
290 295 300 305	
Thr Asn Asp Leu Glu Glu Ser Arg Gln Leu Thr Gln Gln Ile Gln Arg	1079
315 320 325 330	
His Leu Asp Tyr Gln Tyr Ala Leu Arg His Leu Tyr Val Leu Val Asn	1127
335 340 345 350	

372

375

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 ggtgggaaaa cctctctatt gagaaggga atatttctt ttatgggg tgggtgttt 1514
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 Leu Trp Ala Ala Leu Leu Gly Ala Val Ala Leu Arg Pro Ala Glu
 15 20 25 30

gcg gtg tcc gag ccc acg acc gtg gcg ttt gac gtg cgc ccc ggc ggc 146
 Ala Val Ser Glu Pro Thr Thr Val Ala Phe Asp Val Arg Pro Gly Gly
 35 40 45

gtc gtg cat tcc ttc tcc cat aac gtc ggc cgc ggc gac aaa tat acg 194
 Val Val His Ser Phe Ser His Asp Val Gly Pro Gly Asp Lys Tyr Thr
 50 55 60

tat atc ttc atc ttc atc ttc ttc atc ttc atc ttc atc ttc atc ttc 24
 Tyr Met Ile Thr Tyr Ala Ser His Gly Gly Thr Asp Ala Ile Tyr Ile
 65 70

gtg atc ttc atc ttc atc ttc atc ttc atc ttc atc ttc atc ttc atc 31
 Val Ser Ile Gly Ile Ser Val Arg His Ala His Ile Thr Tyr Thr Ile
 80 85 90

tgg agt ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 38
 Trp Arg Ile Glu Gly Lys Ser Tyr Ile Tyr Phe Thr Ala Phe Lys Ala
 95 100 105

a
 ant

gtg atg aaa aca gaa gta gtt gac agt ccc ggg gaa tta aat ttt gat 481
Val Thr Lys Thr Ala Val Ala His Arg Pro Gly Ala His Lys Ala His
141 150 155

atg tta aag atg gta att gta gac aag gaa tgg cgc act gag atg 527
Leu Ser Lys Leu Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu
160 165 170

tgaacagca; cccatgttgag gttggaat tttctatctcc ggtgaagctg aaaggggctg 587
tgcctctca aaccccaaca catcaact aat tttctaggaag gaa tcttca atttcttaca 617
tgggtgagc ttgccttctc cggaggggtt tgaagggctg ctgaagccat ggggagaga 707
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tgtggggaa agcaggaatg ctgctctca tttcagcag agcatctt atgggggga 887
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<220>
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Met Gly Val Lys Leu
1 5

gag ata ttt cgg atg ata ata taa cta act ttc cct gta gta atg ttc 164
Glu Ile Phe Arg Met Ile Ile Tyr Leu Thr Phe Pro Val Ala Met Ile
10 15 20

tgg gtt tcc aat cag gcc gag tgg ttt gag gac gat gtc ata cag cgc 212
Tyr Val Ser Asn Gln Ala Gln Tyr Phe Gln Asp Asp Val Ile Gln Arg
25 30 35

tat ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 26
Tyr Arg His Leu Tyr Phe His Arg Lys Leu Gln His Ile Gln Arg His
40 45 50 55 60

aaa gag aat tta ctt aat gtt gtt gag aag atc ctt ctt ttt ttt 319
Lys Glu Arg Leu Arg Lys Arg Arg Gln Gln Lys Leu Leu Arg Asp Ala
65 70 75 80 85

tat ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 320

4413 - Homo sapiens

4420 -

4421 - CDS

4422 - (754)...(4169)

4400 - 25

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ttcttgatga accttgcttt ttatgggttt ttttttttgc ttaaagaagct gggatttttt 100
attttttttt tcaatgggga tttttttttt tttttttttt at tttttttt tttttttt ttt
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tgtgtttctt gcttgatctt ctgtctgggg tggctcaggt cacaagaaga agctgacccc 300
tcttggtctt gggaaaaatgc tggattcatt gcttgacaca aatgcaaggg ccttccccca 360
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cattcaagag gacttttcag gcatcttga gaaagaacgg cagaacacac agcaaggaaa 720
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Met Arg Pro Phe Phe Leu Leu

1

5

tgt ttt gcc ctg cct ggc ctc ctg cat gcc aaa aaa gcc tgc tcc agt 820
Cys Phe Ala Leu Pro Gly Leu Leu His Ala Gln Gln Ala Cys Ser Arg
10 15 20

ggg gcc tgc tat cca cct gtt ggg gac ctg att gtt ggg agg acc ggg 880
Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu Val Gly Arg Thr Arg
25 30 35

ttt ctc cga gct tca tct acc tgt gga ctg acc aag cct gag acc tat 940
Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys Pro Glu Thr Tyr
40 45 50 55

tgc acc cag tat ggc gag tgg cag atg aaa tgc tgc aag tgt gac tcc 960
Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys Cys Lys Cys Asp Ser
60 65 70

gtt tat att cag att tat tat att att att att att att att att att att 1000
Arg Ala His His Asn Tyr Tyr Asn His Asn Val His Asn Val Ala Ser
75 80 85 90 95 100

ttt ttc ggc acc atg ggt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1060
Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln Asn Asp Val Asn Pro
90 95 100

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1120
Val Ser Leu Gln Leu Asp Leu Asp Asn Asn His His Leu His His Val
105 110 115 120 125 130 135 140 145 150

140

145

150

gac tgc acc tcc acc ttc cct cgg gtc agc cag ggt cgg ctt cag ttc 1254
 Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln Gly Arg Irs Gln Ser
 155 160 165

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 Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln Arg Pro Asn Ala Arg
 170 175 180

cta aat ggg ggg aag gtc caa att aar ctt atg gat tta atg ttt ggg 1350
 Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met Asp Leu Val Ser Gly
 185 190 195

att cca gca att caa agt caa aac att caa cag gty ggg agt att ara 1398
 Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Gln Val Gly Gln Ile Thr
 200 205 210 215

aac ttg aga gtc aat ttc acc agg atg gcc cct gtg ccc caa agg ggc 1446
 Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro Val Pro Gln Arg Gly
 220 225 230

tac cac cct ccc agc gcc tac tat gct gtg tcc cag ctc cgt cta cag 1494
 Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser Gln Leu Arg Leu Gln
 235 240 245

ggg agc tgc ttc tgt cac gcc cat gct gat cgc tgc gca ccc aag cct 1542
 Gly Ser Cys Phe Cys His Gly His Ala Asp Arg Cys Ala Pro Lys Pro
 250 255 260

ggg gcc tct gca gcc ccc tcc acc gct gtg cag gtc cac gat att tgt 1590
 Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val His Asp Val Cys
 265 270 275

gtc tgc cag cac aac act gcc gcc cca aat tgt gag cgc tgt gca ccc 1638
 Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro
 280 285 290 295

tta tta att aat att ctt att att att att att att att att att att 1686
 Phe Tyr Asn Asn Arg Irs Trp Arg Ile Ala Gln Gly Gln Asp Ala His
 300 305 310 315 320 325 330 335 340 345 350 355 360

tta tta cca agg tgc gat tgc att att att att att att att att att 1734
 Gln Cys Gln Arg Cys Asp Cys Asn Gly His Ser Gln Thr Cys His Ile
 315 320 325

tta tta att att att att att att att att att att att att att att 1782
 Arg Ile Ala Val Ile Ala Ala Ser Gln Arg Asn Tyr Gly Gly Val Tyr
 365 370 375 380 385 390 395 400 405 410 415 420 425

tta tta att att att att att att att att att att att att att att 1830
 Arg Ile Ala Val Ile Ala Ala Ser Gln Arg Asn Tyr Gly Gly Val Tyr
 430 435 440 445 450 455 460 465 470 475 480 485 490

tgc atc tcc tgc gag tgt gat ccg gat ggg gca gtg cca ggg gct ccc 1926
Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala Val Pro Gly Ala Pro
380 385 390

tgt gac cca gtg acc ggg cag tgt gtg tgc aag gag cat gtg cag gga 1974
Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys Glu His Val Gln Gly
395 400 405

gag cgc tgt gac cta tgc aac ccg ggc ttc act cca ctc acc tac ggc 2022
Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr Gly Leu Thr Tyr Ala
410 415 420

aac ccg cag ggc tgc cac cgc tgt gac tgc aac atc ctg ggg tcc cgg 2070
Asn Pro Gln Gly Cys His Arg Cys Asp Cys Asn Ile Leu Gly Ser Arg
425 430 435

agg gac atg ccg tgt gac gag gag agt ggg cgc tgc ctt tgt ctg ccc 2118
Arg Asp Met Pro Cys Asp Glu Glu Ser Gly Arg Cys Leu Cys Leu Pro
440 445 450 455

aac gtg gtg ggt ccc aaa tgt gac cag tgt gct ccc tac cac tgg aag 2166
Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro Tyr His Trp Lys
460 465 470

ctg gcc agt ggc cag ggc tgt gaa ccg tgt gcc tgc gac ccg cac aac 2214
Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys Asp Pro His Asn
475 480 485

tcc ctc agc cca cag tgc aac cag ttc aca ggg cag tgc ccc tgt cgg 2262
Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln Cys Pro Cys Arg
490 495 500

gaa ggc ttt ggt ggc ctg atg tgc agc gct gca gcc atc cgc cag tgt 2310
Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala Ile Arg Gln Cys
505 510 515

cca gac cgg acc tat gga gac gca gca aca gga tgc cca gcc tat gac 2358
Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys Arg Ala Cys Arg
520 525 530 535

tgc gac ttc ttc ttc aca ggc ttc ttc ttc ttc ttc ttc ttc ttc ttc 2406
Cys Arg Phe Arg Gly Thr Gln Gly Phe Gly Cys Arg Gln Ala Ser Gly
540 545 550

cgc tgc ctc tgc cgc cct ggc ttg acc ggg ccc cgc tgt gac cag tgc 2454
Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg Cys Asp Gln Cys
555 560 565

a!
ant

ggg aga atg agt aat gaa aac gac agc atg tgg taa ggg aat gaa atg 2598
Gly Arg Leu Arg Asn Ala Thr Ala Ser Leu Trp Ser Gly Pro Gly Leu
600 605 610 615

gag gag agt ggt atg gaa taa agt atc ata gat gaa aag agt aag att 2646
Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala Lys Ser Lys Ile
620 625 630

gag cag atc cga gaa gtt ctc agc agc ccc gaa gtc aca gag cag gag 2694
Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val Thr Gln Gln Gln
635 640 645

gtg gct cag gtc gat agt gac atc atc taa atc aga gaa aat atc cag 2742
Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg Arg Thr Leu Gln
650 655 660

ggc atg cag atg gat atg ccc atg gag gag gag aag ttg tcc att cag 2790
Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr Leu Ser Leu Pro
665 670 675

aga gac atg gag agt ctt gac gaa agt ttc aat agt ctc att aat atg 2838
Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly Leu Leu Thr Met
680 685 690 695

tat cag agg aag agg gag cag ttt gaa aaa ata agc agt gct gat cct 2886
Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser Ser Ala Asp Pro
700 705 710

a
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Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr Glu Gln Ser Ala Gln
715 720 725

gct gct cag cag gtc tcc gac agc tgc cgc att ttg gac cag ctc agg 2982
Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu Asp Gln Leu Arg
730 735 740

gac agc cgg aca gag gaa gag agt atg gtc atg gag gag gaa gaa gaa 3030
Asp Ser Arg Arg Gln Ala Gln Arg Leu Val Arg Ala Ala Gly Gly Gly
745 750 755

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Lys Lys Thr Lys Ser Ile Lys Leu Val Ala Leu Arg Leu Ile Ser Ser
760 765 770

ttg ttg att gat atg aca gaa gaa ttc aac aac ttc agt gtt att ttt 3126
Ser Leu Ile Asp Leu Thr Pro Thr Phe Asn Lys Leu Cys Gly Asp Ser
775 780 785

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 3174
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
790 795 800

200

aac agc ggc aac gac gag aac cta ggc aac ggt tat ggc aac gac cta 266
 Asn Ser Ala Asn Asp Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu
 30 35 40

ctt aat gga ggc aag ctg atg ggc gag aca ccc gag gag aac ctg tta 314
 Leu Asn Gly Val Lys Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe
 45 50 55

act ccc att cta att cta att cta att cta att cta att cta att cta att 322
 Thr Arg Ile Leu Thr Val Gly Pro Gln Ser Leu Gly Ser Glu Ala Leu
 60 65 70 75

ggt tcc ccg acc ggc aga ggc ggt tat aac ggc ttt aat gac aac ggc 330
 Ala Ser Pro Thr Arg Arg Ala Ala Cys Thr Val Phe Thr Ala Thr Ala
 80 85 90

agc aat agg acc tgg ggc cct ccc ctg ccg cat tcc cta aat ggc tgt 338
 Ser Thr Arg Thr Trp Gly Pro Pro Leu Pro His Ser Leu Thr Gly Cys
 95 100 105

gta ttt att gag tgg ttc gtt ttc cct tgt ggc ttg gag aca ttc 346
 Val Phe Ile Glu Trp Phe Val Phe Pro Cys Gly Leu Glu Pro Phe
 110 115 120

cal.

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 <113> Homo sapiens

<214>
 <215> CDS
 <222> (73)...(597)

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 Met Glu Lys Ile Leu Val Ser Ala Ile Leu Leu Leu Val

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Arg Gly Trp Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Gln Gln Ala			
55	55	60	
cta tat gaa tgg ggg gaa agc aac aaa gtt ttg atg att att cat cac	308		
Leu Tyr Lys Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His			
65	70	75	
ttg gat gag tgc cca cac agt caa gct tta aag aaa gtg ttt gct gaa	351		
Leu Asp Glu Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu			
80	85	90	
aat aaa gaa atc ggg aaa ttg gca gag ggg ttt gtc ctc ctc aat ctg	394		
Asn Lys Glu Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu			
95	100	105	
gtt tat gaa aca aat gac aaa cac ctt tct cct gat ggc cag tat gtc	447		
Val Tyr Glu Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val			
110	115	120	125
ccc agg att atg ttt gtt gac cca tct ctg aca gtt aga gcc gat atc	495		
Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile			
130	135	140	
act gga aga tat tca aac cgt ctc tat gct tac gaa cct gca gat aca	543		
Thr Gly Arg Tyr Ser Asn Arg Leu Tyr Ala Tyr Glu Pro Ala Asp Thr			
145	150	155	
gct ctg ttg ctt gac aac atg aag aaa gct ctc aag ttg ctg aag aat	591		
Ala Leu Leu Leu Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr			
160	165	170	
gaa ttg taagaagaaa aaatctcaca gccctctctgt atgtaagga ttgagacttg	647		
Glu Leu			
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